

SEQUENCE LISTING

<110> Brett P. Monia
Mark J. Graham

<120> MODULATION OF DIACYLGLYCEROL ACYLTRANSFERASE 1 EXPRESSION

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<150> US 10/394,808

<151> 2003-03-21

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 Met Gly Asp Arg Gly Ser Ser Arg Arg Arg Arg Thr Gly Ser Arg
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 Pro Ser Ser His Gly Gly Gly Gly Pro Ala Ala Ala Glu Glu Glu Val
 20 25 30
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 Arg Asp Ala Ala Ala Gly Pro Asp Val Gly Ala Ala Gly Asp Ala Pro
 35 40 45
 gcc ccg gcc ccc aac aag gac gga gac gcc ggc gtg ggc agc ggc cac 433
 Ala Pro Ala Pro Asn Lys Asp Gly Asp Ala Gly Val Gly Ser Gly His
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 tgg gag ctg agg tgc cat cgc ctg cag gat tct tta ttc agc tct gac 481
 Trp Glu Leu Arg Cys His Arg Leu Gln Asp Ser Leu Phe Ser Ser Asp
 65 70 75
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 Ser Gly Phe Ser Asn Tyr Arg Gly Ile Leu Asn Trp Cys Val Val Met
 80 85 90 95
 ctg atc ttg agc aat gcc cgg tta ttt ctg gag aac ctc atc aag tat 577
 Leu Ile Leu Ser Asn Ala Arg Leu Phe Leu Glu Asn Leu Ile Lys Tyr
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 ggc atc ctg gtg gac ccc atc cag gtg gtt tct ctg ttc ctg aag gat 625
 Gly Ile Leu Val Asp Pro Ile Gln Val Val Ser Leu Phe Leu Lys Asp
 115 120 125
 ccc cat agc tgg ccc gcc cca tgc ctg gtt att gcg gcc aat gtc ttt 673
 Pro His Ser Trp Pro Ala Pro Cys Leu Val Ile Ala Ala Asn Val Phe
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 gct gtg gct gca ttc cag gtt gag aag cgc ctg gcg gtg ggt gcc ctg 721
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 acg gag cag gcg gga ctg ctg ctg cac gta gcc aac ctg gcc acc att 769
 Thr Glu Gln Ala Gly Leu Leu Leu His Val Ala Asn Leu Ala Thr Ile
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 180 185 190

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Val Gly Ser Leu Leu Ala Leu Met Ala His Thr Ile Leu Phe Leu Lys	
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Lys Ala Ala Ser Ala Gly Lys Lys Ala Ser Ser Ala Ala Ala Pro His	
225 230 235	
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Thr Val Ser Tyr Pro Asp Asn Leu Thr Tyr Arg Asp Leu Tyr Tyr Phe	
240 245 250 255	
ctc ttc gcc ccc acc ttg tgc tac gag ctc aac ttt ccc cgc tct ccc	1057
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Ile Gln Asn Ser Met Lys Pro Phe Lys Asp Met Asp Tyr Ser Arg Ile	
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Glu Ser Val Thr Tyr Phe Trp Gln Asn Trp Asn Ile Pro Val His Lys	
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Trp Cys Ile Arg His Phe Tyr Lys Pro Met Leu Arg Arg Gly Ser Ser	
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Thr Gly Met Met Ala Gln Ile Pro Leu Ala Trp Phe Val Gly Arg Phe	
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Phe Gln Gly Asn Tyr Gly Asn Ala Ala Val Trp Leu Ser Leu Ile Ile	
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Gly Gln Pro Ile Ala Val Leu Met Tyr Val His Asp Tyr Tyr Val Leu	
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Asn Tyr Glu Ala Pro Ala Ala Glu Ala	
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 Met Gly Asp Arg Gly Gly
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ggc tac tgg gat ctg agg tgc cat cgt ctg caa gat tct ttg ttc agc Gly Tyr Trp Asp Leu Arg Cys His Arg Leu Gln Asp Ser Leu Phe Ser 75 80 85	353
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Met Val Pro Thr Ile Gln Asn Ser Met Lys Pro Phe Lys Asp Met Asp	
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Tyr Ser Arg Ile Ile Glu Arg Leu Leu Lys Leu Ala Val Pro Asn His	
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Pro Val His Lys Trp Cys Ile Arg His Phe Tyr Lys Pro Met Leu Arg	
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His Gly Ser Ser Lys Trp Val Ala Arg Thr Gly Val Phe Leu Thr Ser	
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Ala Phe Phe His Glu Tyr Leu Val Ser Val Pro Leu Arg Met Phe Arg	
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455 460 465 470	
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Thr Leu Ile Ile Gly Gln Pro Val Ala Val Leu Met Tyr Val His Asp	
475 480 485	

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 Ala Gly Ser Ser Arg Arg Arg Arg Thr Gly Ser Arg Val Ser Val Gln
 10 15 20

gga ggt agt ggg ccc aag gta gaa gag gac gag gtg cga gaa gcg gct	149
Gly Gly Ser Gly Pro Lys Val Glu Glu Asp Glu Val Arg Glu Ala Ala	
25 30 35	
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Val Ser Pro Asp Leu Gly Ala Gly Gly Asp Ala Pro Ala Pro	
40 45 50	
gct cca gcc cat acc cgg gac aaa gac cgg cag acc agc gtg ggc gac	245
Ala Pro Ala His Thr Arg Asp Lys Asp Arg Gln Thr Ser Val Gly Asp	
55 60 65 70	
ggc cac tgg gag ctg agg tgc cat cgt ctg caa gac tct ttg ttc agc	293
Gly His Trp Glu Leu Arg Cys His Arg Leu Gln Asp Ser Leu Phe Ser	
75 80 85	
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Ser Asp Ser Gly Phe Ser Asn Tyr Arg Gly Ile Leu Asn Trp Cys Val	
90 95 100	
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Val Met Leu Ile Leu Ser Asn Ala Arg Leu Ser Leu Glu Asn Leu Ile	
105 110 115	
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Lys Tyr Gly Ile Leu Val Asp Pro Ile Gln Val Val Ser Leu Phe Leu	
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Lys Asp Pro Tyr Ser Trp Pro Ala Pro Cys Leu Ile Ile Ala Ser Asn	
135 140 145 150	
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Ile Phe Ile Val Ala Thr Phe Gln Ile Glu Lys Arg Leu Ser Val Gly	
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Ala Leu Thr Glu Gln Met Gly Leu Leu Leu His Val Val Asn Leu Ala	
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Thr Ile Ile Cys Phe Pro Ala Ala Val Ala Leu Leu Val Glu Ser Ile	
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Thr Pro Val Gly Ser Leu Phe Ala Leu Ala Ser Tyr Ser Ile Ile Phe	
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Arg Val Lys Ala Lys Ala Val Ser Ala Gly Lys Lys Val Ser Gly Ala	
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Pro	Arg	Ser	Pro	Arg	Ile	Arg	Lys	Arg	Phe	Leu	Leu	Arg	Arg	Val	Leu	
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Thr	Leu	Ile	Ile	Gly	Gln	Pro	Val	Ala	Val	Leu	Met	Tyr	Val	His	Asp	
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